

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 3, 2000, 14:17:29 : Search time 49779.6 Seconds
(without alignments)
-75.331 Million cell updates/sec

Title: US-08-962-560A-3

Perfect score: 1235
Sequence: 1 CGAGGCTCAGCTCCGGCG.....AGAAAAAAAAAAAAAAAA 1235

Scoring table: IDENTITY_NDC
Gapop 10.0, Gapext 1.0

Searched: 821193 seqs, -1518192014 residues

Total number of hits satisfying chosen parameters: 1642386

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pl3:*
10: gb_pl4:*
11: gb_pl5:*
12: gb_pl6:*
13: gb_pl7:*
14: gb_pl8:*
15: gb_pl9:*
16: gb_pl10:*
17: gb_pl11:*
18: gb_pl12:*
19: gb_pl13:*
20: gb_pl14:*
21: gb_pl15:*
22: gb_pl16:*
23: gb_pl17:*
24: gb_pl18:*
25: gb_pl19:*
26: gb_pl20:*
27: gb_pl21:*
28: gb_pl22:*
29: gb_pl23:*
30: gb_pl24:*
31: gb_pl25:*
32: gb_pl26:*
33: gb_pl27:*
34: gb_pl28:*
35: gb_pl29:*
36: gb_pl30:*
37: gb_pl31:*
38: gb_pl32:*
39: gb_pl33:*
40: gb_pl34:*
41: gb_pl35:*
42: gb_pl36:*
43: gb_pl37:*
44: gb_pl38:*

45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1218	98.6	13812	12	MMPRMGNS
2	1119.2	90.6	1185	12	MMU88325
3	1117.8	90.5	1193	12	AFI120490
4	1098.4	88.9	1177	12	AFI180302
5	1086	87.9	13187	12	BRPMTNP2
6	1051.2	85.1	1056	12	AB000677
7	904.2	73.2	909	12	AB000710
8	725.6	58.8	12589	40	AC002286
9	723.6	58.8	25417	32	HSAC002047
10	723.6	58.6	175950	33	AC007220
11	718.6	58.2	1215	9	AB000734
12	690.2	55.9	1094	10	HSU089326
13	682.4	55.3	1082	9	AB005043
14	623.2	50.5	1030	9	AB000676
15	571.6	46.3	908	40	AFI132440
16	473.4	38.3	11270	41	AC009140
17	101.4	8.2	850	9	AB004904
18	95.6	7.7	678	9	AB006957
19	94	7.6	682	40	AFI159654
20	93.2	7.5	2792	12	RNO249240
21	91.4	7.4	2187	12	MMU88328
22	90.8	7.4	863	12	AF075383
23	82.2	6.7	1262	4	AFI167297
24	69.6	5.6	774	5	AR035856
25	69.6	5.6	774	5	AR035856
26	69.6	5.6	1960	5	AR035809
27	69.6	5.6	1960	5	AR035836
28	69.6	5.6	2198	40	AFI132297
29	64	5.2	181634	44	AC016253
30	62.4	5.1	22861	11	HSU0C42
31	62.2	5.0	67960	44	AC016188
32	61	4.9	56870	32	CEY3986_3
33	60.4	4.9	171653	32	HS11167H4
34	60.4	4.9	173721	43	AC015866
35	59.6	4.8	108064	41	AC010404
36	59.4	4.8	110000	45	AC017014_1
37	58.8	4.8	148754	44	AC013648
38	58.4	4.7	46108	91	AC011100
39	58.2	4.7	4839	9	HDMOPIDORE
40	58.2	4.7	107475	45	AC017106
41	58	4.7	64096	44	AC015468
42	57.8	4.7	840	8	CNS01BNS
43	57.6	4.7	181634	44	AC016253
44	57.4	4.6	1964	2	SC2C1A
45	57.4	4.6	77671	43	AC013505

ALIGNMENTS

RESULT 1
LOCUS MMPRMGNS 13812 bp DNA
DEFINITION M.musculus PRM1, PRM2, PRM3 and TNP1 genes.
ACCESSION Z47352
VERSION 247352.1 GI:1360004
KEYWORDS PRM1 gene; PRM2 gene; PRM3 gene; protamine; TNP2 gene; transition

11-DEC-1996

SOURCE	protein 2.
ORGANISM	house mouse.
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
TITLE	Rodentia; Sciurgnathhi; Muridae; Murinae; Mus.
JOURNAL	1 (bases 1 to 13812)
REFERENCE	Schluter,G. and Engel,W.
AUTHORS	Genomic sequence of the mouse protamine gene cluster
TITLE	Unpublished
JOURNAL	2 (bases 1 to 13812)
REFERENCE	Schluter,G.
AUTHORS	Direct Submission
TITLE	Submitted (05-JUN-1995) Schluter G., Institut fuer Humanogenetik,
JOURNAL	Universitaet Goettingen, Gosslerstr.12d, Goettingen, germany, 37073
REFERENCE	4 (bases 1 to 13812)
AUTHORS	Schluter,G., Celik,A., Obata,R., Schlicker,M., Hofferbert,S.,
TITLE	Schlung A., Adham,I.M. and Engel,W.
JOURNAL	Sequence analysis of the conserved protamine gene cluster shows
REFERENCE	that it contains a fourth expressed gene
AUTHORS	Mei. Reprod. Dev. 43 (1), 1-6 (1996)
TITLE	On Jun 5, 1996 this sequence version replaced gi:1886891.
JOURNAL	Related sequences: X07625, X07626, M60254.
MEDLINE	
COMMENT	
FEATURES	
SOURCE	Location/Qualifiers
gene	1..13812
CDS	/organism="Mus musculus"
gene	/strain="C129"
CDS	/db_xref="taxon:10090"
gene	/chromosome="16"
CDS	653..902
gene	/gene="Prml"
CDS	join(653..758,853..902)
gene	/gene="Prml"
CDS	/note="male germcell specific, haploid expressed;
gene	chromatin binding"
CDS	/codon_start=1
gene	/product="protamine 1"
CDS	/protein_id="CA87410.1"
gene	/db_xref="GI:1360005"
CDS	/db_xref="SWISS-PROT:P02319"
gene	/translation="MARYRCRSKRSRRCRRRRRCRRRRRCRRRRRCRRRRRC
CDS	TIKKKKY"
gene	5189..5817
CDS	/gene="Prm2"
gene	join(5389..5647,5753..5817)
CDS	/gene="Prm2"
gene	/note="Description: male germcell specific, haploid
CDS	expressed; chromatin binding"
gene	/codon_start=1
CDS	/product="protamine 2"
gene	/protein_id="CA87411.1"
CDS	/db_xref="GI:1360006"
gene	/db_xref="SWISS-PROT:P07978"
CDS	/translation="WVYRMRSPSGHGPGODHEREEQGGSLSPERYEDYGRTH
gene	RGHHRHRCRSKRRLRIHKRRRSRRRRHRCRRRRRCRRRRRCRRRCRCRC
CDS	RRHHH"
gene	6498..6806
CDS	/gene="Prm3"
gene	6498..6806
CDS	/gene="Prm3"
gene	/note="male germcell specific, haploid expressed"
CDS	/codon_start=1
gene	/product="protamine 3"
CDS	/protein_id="CA87412.1"
gene	/db_xref="GI:1360007"
CDS	/db_xref="SWISS-PROT:Q62100"
gene	/translation="MGSRCRSLSTGHDPQAPONTGHNHGHSNMKTLVACVSODNFSLS

gene	8786..9310
CDS	/gene="tnp2" join(8786..9122,9294..9310) /gene="tnp2" /note="male germcell specific, haploid expressed; chromatin binding" /codon_start=1 /product="transition protein 2" /protein_id="CA87413.1" /db_xref="GI:1360008" /db_xref="Swiss-Prot:P11378" /translation="MDTKMOSLPTTHPHSSSNPOHSNOCNOCYCSHHKRCSSQAGHSSSPSPGPMKPKPVSVSRHSRSPAPSRHSGSCPKNRKTFEGKIVSRKAVRRKRRIHAKRKRTSGRRYK"
BASE COUNT	3400 a 3514 c 3869 g 3029 t
ORIGIN	
Query Match	98.6% Score 1218; DB 12; Length 13812;
Best Local Similarity	99.6% Pred. No. 2.6e-210;
Matches 1221; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
1	CGAGGCTCAAGCTCCGGGCGGATTCCTGCTCCGCTCCGCTCCTTGGGGTCCTGTGGCC 60
12356	CGAGGCTCAAGCTCCGGGCGGATTCCTGCTCCGCTCCGCTCCTTGGGGTCCTGTGGCC 12415
61	GGCCGTGCGAACCCGGAGCGCCGGGCTACGTCGTCGTCTCCCATCAGGAGGAGCCCG 120
12416	GGCCGTGCGAACCCGGAGCGCCGGGCTACGTCGTCGTCTCCCATCAGGAGGAGCCCG 12475
121	GACGCTATGCGCCACCCCTCCAGCTGGCCCTCGAGTAGATGATGATGACGCAACAGAGT 180
12476	GACGCTATGCGCCACCCCTCCAGCTGGCCCTCGAGTAGATGATGATGACGCAACAGAGT 12535
181	GGCAGCCGCAACATCGATCTCCCGGAGAGACCCCGACGGGGGTGACAGCCCTCTCTC 240
12536	GGCAGCCGCAACATCGATCTCCCGGAGAGACCCCGACGGGGGTGACAGCCCTCTCTC 12595
241	GTCCTGCTCTGTCCTCTCGCAGCGGGCCCGCTGCTCCCGGCGCTCCGCGGCGGTCCC 300
12596	GTCCTGCTCTGTCCTCTCGCAGCGGGCCCGCTGCTCCCGGCGCTCCGCGGCGGTCCC 12655
301	AGCCCCAGCCCCCTGGCGACATCTCCGACACTTCGCTCCGCTCCGACTTCGATTACGGCG 360
12656	AGCCCCAGCCCCCTGGCGACATCTCCGACACTTCGCTCCGCTCCGACTTCGATTACGGCG 12715
361	CATCAGCGGACAGCGCGCTCTCGAGCGCTTGCGGCTTCTATTGGGGAGACCCCTGAGAGT 420
12716	CATCAGCGGACAGCGCGCTCTCGAGCGCTTGCGGCTTCTATTGGGGAGACCCCTGAGAGT 12775
421	GCACGGGGCGCAGAGCGGCTGCTGCCGAGACCCGCGGACACTTCTTGGTGGCGGACAG 480
12776	GCACGGGGCGCAGAGCGGCTGCTGCCGAGACCCGCGGACACTTCTTGGTGGCGGACAG 12835
481	TGCGTCAACGGAACGCTCTTCGCGCTCAGCGGTGAATAGGCTTCGGGGCCCGACAGACAT 540
12836	TGCGTCAACGGAACGCTCTTCGCGCTCAGCGGTGAATAGGCTTCGGGGCCCGACAGACAT 12895
541	CCGCGTGCACCTTCAGGCGCGGCCCTTTCACATTGGAGGGAGCGCGCAGACACTTCGACTG 600
12896	CCGCGTGCACCTTCAGGCGCGGCCCTTTCACATTGGAGGGAGCGCGCAGACACTTCGACTG 12955
601	CCTTTTCGAGCTGCTGAGACACTACGTGGCGGGCGCGCGCGCAGCTGTTGGGGGCCCGCT 660
12956	CCTTTTCGAGCTGCTGAGACACTACGTGGCGGGCGCGCGCGCAGCTGTTGGGGGCCCGCT 13015
661	GGCGCAAGCGCGGCTGGGGCGCGTGCAGAGAGCTGTGTCGGCAGAGGACATCGTGGCGCGCGT 720
13016	GGCGCAAGCGCGGCTGGGGCGCGTGCAGAGAGCTGTGTCGGCAGAGGACATCGTGGCGCGCGT 13075
721	GGGTGCGAGAACCTGGCGGCGCATCCCTCTTAACCCGCGTACTCGTACTACCTGACTTC 780

Dh	13076	GGGTGCGAGAACTGGCGCGACTCCCTCTTAACCGGGTACTCCGGACTACCTGAGTTC	13135
Qy	781	CTTCCCTTCCAGANCTGACCGGGCTGGCGCTGTCCGCGACATTAAAGTGGGGCGCCTTA	840
Dh	13136	CTTCCCTTCCAGANCTGACCGGGCTGGCGCTGTCCGCGACATTAAAGTGGGGCGCCTTA	13195
Qy	841	TTATTTCTTATTAATTAATTAATTAATTTCTTGGAACACAGTGGGAGCGCTCCCGGCT	900
Dh	13136	TTATTTCTTATTAATTAATTAATTAATTTCTTGGAACACAGTGGGAGCGCTCCCGGCT	13255
Qy	901	GGGTGCGAGGAGTGGTGTGTGGAGGGTGAGATGCCTCCACTTGTGGCTGGAGACTCAT	960
Dh	13256	GGGTGCGAGGAGTGGTGTGTGGAGGGTGAGATGCCTCCACTTGTGGCTGGAGACTCAT	13315
Qy	961	CCCACCTCTCAGGGGTGGGGGTGCTCCCTCCTGGTGTCTCCTCCGGGTCCCGCCGTGT	1020
Dh	13316	CCCACCTCTCAGGGGTGGGGGTGCTCCCTCCTGGTGTCTCCTCCGGGTCCCGCCGTGT	13375
Qy	1021	GTAGACGCTGTGTGTGGGGGCCAGGACCGATTCACACGTCACGTCACAGTTTAACT	1080
Dh	13376	GTAGACGCTGTGTGTGGGGGCCAGGACCGATTCACACGTCACGTCACAGTTTAACT	13435
Qy	1081	ATTCCAGATCTTTGCACAAACCAAGGGGTCCGGGAGGGTCTGTGGCTCATTTTCTGC	1140
Dh	13436	ATTCCAGATCTTTGCACAAACCAAGGGGTCCGGGAGGGTCTGTGGCTCATTTTCTGC	13495
Qy	1141	TGTGCAGAATATCTATTTTAAATTTTAAACGCCAGTTAGGTAAATAAATTATATGA	1200
Dh	13496	TGTGCAGAATATCTATTTTAAATTTTAAACGCCAGTTAGGTAAATAAATTATATGA	13555
Qy	1201	AAGTTTTTTTTTAAAGAAAAAAA 1226	
Dh	13556	AAGTTTTTTTTTAAAGAAAAAAA 13581	

```

RESULT 2
MMU088325
LOCUS      MMU088325      1185 bp      mRNA      06-JUL-1997
DEFINITION Mus musculus suppressor of cytokine signalling-1 (SOCS-1) mRNA,
complete cds.
ACCESSION U88325
VERSION   U88325.1  GI:2245381
KEYWORDS
SOURCE    house mouse.
           Mus musculus
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
           Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1185)
           Starr,R., Willison,T.A., Viney,E.M., Murray,L.J.L., Rayner,T.R.,
           Jenkins,B.J., Gonda,T.J., Alexander,W.S., Metcalf,D., Nicola,N.A.
           and Hilton,D.J.
           A family of cytokine-inducible inhibitors of signalling
           Nature 387 (6636), 917-921 (1997)
           97345633
TITLE     TITLE
JOURNAL   JOURNAL
MEDLINE   MEDLINE
REFERENCE 2. (bases 1 to 1185)
           Starr,R., Willison,T.A., Viney,E.M., Murray,L.J.L., Rayner,T.R.,
           Jenkins,B.J., Gonda,T.J., Alexander,W.S., Metcalf,D., Nicola,N.A.
           and Hilton,D.J.
           Direct Submmission
           Submitted (04-FEB-1997) Cancer Research Unit, The Walter and Eliza
           Hall Institute of Medical Research, PO Royal Melbourne Hospital,
           VIC 3050, Australia
           location/Qualifiers
FEATURES
SOURCE    1. 1185
           /organism="Mus musculus"
           /db_xref="taxon:10090"
           /chromosome="16"
           /tissue_type="thymus"
           119. .757
           /gene="SOCS-1"
           119. .757
           /gene="SOCS-1"
CDS

```

```

/codon_start=1
/product="suppressor of cytokine signaling-1"
/protein_id="AA82400.1"
/db_xref="GI:2245382"
/translation="MVARNQVAAADNAISPAAPRRRSESSSSSSSPAAPVRDPCE
AVPAPAGDTHFTFRFSHSDYRTTRTSGADGCFWPGSVYSGAEERLAEAVGTEF
LVRSRORNCFFALSVAMSGPRTIRVHFOALDAGGDSRTSPGCEILHEHYAADR
RMGACPIRRRVRVRIQDLCGRQRYIAAAGRENLAIPNPVLDLSSPPQI"
BASE COUNT      103 a      413 c      334 g      255 t
ORIGIN

```

Query Match	90.6%	Score 119.2	DB 12	Length 1185
Best Local Similarity	97.2%	Pred. No. 118-192		
Matches 1139	Conservative 0	Mismatches 33	Indels 0	Gaps 0
QY 56	TGGCCGCGCTGTGCGACCCGGACGCGCCGGCTCAGTGCCTCTGTCTCCCCATCAGCGCAG	115		
Db 14	TGGCGGACAGCGCGCCCGGAGGCCCGCCAGCGCGGGGTCCCGGCTCTCCCGCAGCGCAG	73		
QY 116	CCCCGGACGCTATGGCCACCCTTCAGCTGGCCCTTGAAGATGTAGACGCAAC	175		
Db 74	CCCCGGAGCTATGGCCACCCTTCAGCTGGCCCTTGAAGATGTAGACGCAAC	133		
QY 176	CAGGGGAGCGCGAATAGCATTCGCCCGGAGAGAGGCCCGGACGGCGGCGAAGGCC	235		
Db 134	CAGGGGAGCGCGAATAGCATTCGCCCGGAGAGAGGCCCGGACGGCGGCGAAGGCC	193		
QY 236	TCTCTGTCCTGTCTCTCTCTCCCGCAGCGGCCCGCGTCCCGCGGCTCCGCGCGG	295		
Db 194	TCTCTGTCTGTCTGTCTCTCTCTCCCGCAGCGGCCCGCGTCCCGCGGCTCCGCGCGG	253		
QY 296	GTCGCCAGCCCAAGCCCTGCGGACACTCTTCGACCTTCGCTCCGCTCCGATTC	355		
Db 254	GTCGCCAGCCCAAGCCCTGCGGACACTCTTCGACACTTCGCTCCGCTCCGATTC	313		
QY 356	CGGGGACATCAGCGGAGACCGCGGCTCTGTGAGCGCTGCGGCTCTATGGGAGCCCGT	415		
Db 314	CGGGGACATCAGCGGAGACCGCGGCTCTGTGAGCGCTGCGGCTCTATGGGAGCCCGT	373		
QY 416	AGCGTGACGGGGGCGACAGCGGCTGCGTCCGACGCCGCTGGGACACTTCTGGTGGC	475		
Db 374	AGCGTGACGGGGGCGACAGCGGCTGCGTCCGACGCCGCTGGGACACTTCTGGTGGC	433		
QY 476	GACAGTCGTCAACGGAACCTGCTTTCGCGCTCAGCGGTGAAGATGCTTCGGGCCACG	535		
Db 434	GACAGTCGTCAACGGAACCTGCTTTCGCGCTCAGCGGTGAAGATGCTTCGGGCCACG	493		
QY 536	AGCATCCGCGTGTGACATTCGAGCGCGGCGGCTTCCACTTGAACGGCAGCGGACCTTC	595		
Db 494	AGCATCCGCGTGTGACATTCGAGCGCGGCGGCTTCCACTTGAACGGCAGCGGACCTTC	553		
QY 596	GACAGCTTTTGAAGCTGTGAGACACTAGCTGGGCGGCGCGCGGCTATTTGGGGGC	655		
Db 613	GACAGCTTTTGAAGCTGTGAGACACTAGCTGGGCGGCGCGCGGCTATTTGGGGGC	613		
QY 715	CCGCTGCGCCAGCGCGCGGCTGCGGCGGCTGAGAGAGCTGTTCGCCAGCGCATGTGCGC	715		
Db 673	CCGCTGCGCCAGCGCGCGGCTGCGGCGGCTGAGAGAGCTGTTCGCCAGCGCATGTGCGC	673		
QY 775	GCGGTGGGTGCGAGAACCTGGCGCGCATCCCTTTAACCCGGTACTCCGTGACTCTG	775		
Db 733	GCGGTGGGTGCGAGAACCTGGCGCGCATCCCTTTAACCCGGTACTCCGTGACTCTG	733		
QY 835	AGTTCCTTCCCTTCGAGATTCGACCGCGCTGCGCTGCGCGCAGCATTAAGTGGGGCG	835		
Db 793	AGTTCCTTCCCTTCGAGATTCGACCGCGCTGCGCTGCGCGCAGCATTAAGTGGGGCG	793		
QY 895	CCTATTATTCTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT	895		
Db 853	CCTATTATTCTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT	853		
QY 955	CGCGTGGGTGCGAGGAGGTGTGAGAGGTGAGATGCTCCACCTTCTGGCTGGAGAC	955		

|||||
Db 854 GCGCTGGGTCGAGGAGAGGTGTGTGAGAGGTGAGATGCTCCCACTTGTGGCTGGAGAC 913
OY 956 CTCATCCCACTCTCAAGGGGTGGGGTGTCTCCCTTCCTGCTGCTCCTCCGGGTCCCCC 1015
Db 914 CTCATCCCACTCTCAAGGGGTGGGGTGTCTCCCTTCCTGCTGCTCCTCCGGGTCCCCC 973
OY 1016 TGGTGTGACACCTGTGTCTGGGGCAGAGCACTGAATTCACCTCCTACCTCCATGTT 1075
Db 974 TGGTGTGACACCTGTGTCTGGGGCAGAGCACTGAATTCACCTCCTACCTCCATGTT 1033
OY 1076 TACATATTCAGATATCTTTGCAACAACCGAGGGTGGGGAGGCTCTGAGCTCATTTT 1135
Db 1034 TACATATTCAGATATCTTTGCAACAACCGAGGGTGGGGAGGCTCTGAGCTCATTTT 1093
OY 1136 TCTGCTGTGCAAAATATCTATTTATTTATTTTACAGCCAGTTAGTAAATCTTTAT 1195
Db 1094 TCTGCTGTGCAAAATATCTATTTATTTATTTTACAGCCAGTTAGTAAATCTTTAT 1153
OY 1196 TATGAAGTTTATTTTAAAAAGAAAAAAA 1227
Db 1154 TATGAAGTTTATTTTAAAAAGAAAAAAA 1185

RESULT 3
AF120490 1193 bp mRNA ROD 10-AUG-1999
LOCUS AF120490 Mus musculus suppressor of cytokine signalling-1 (Socs1) mRNA,
DEFINITION complete cds.
ACCESSION AF120490.1 GI:4581880
VERSION AF120490.1 GI:4581880
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS De Sepulveda, P., Okkenhaug, K., La Rose, J., Hawley, R.G., Dubreuil, P.,
TITLE Socs1 binds to multiple signalling proteins and suppresses steel
factor-dependent proliferation
JOURNAL EMO J. 18 (4), 904-915 (1999)
MEDLINE 99146908
REFERENCE 2 (bases 1 to 1193)
AUTHORS De Sepulveda, P. and Rottepel, R.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-1999) Experimental Therapeutics, Ontario Cancer
Institute, 610 University Avenue, Toronto, ON M5G 2M9, Canada
FEATURES
source
1. .1193
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="16"
/cell_line="EML-Cl"
1. .1193
/gene="Socs1"
130. .768
/gene="Socs1"
/note="Socs-1"
/codon_start=1
/product="suppressor of cytokine signalling-1"
/protein_id="A02477.1"
/db_xref="GI:4581881"
/translation="MVARNVADNNAISPAEPRRSPSSSSSSSPAPAVRPPCP
AVPAPGDFHFRFSHSDYRITRTSALDAGFTWGPISVGAHERLAEEVGF
LVRSROBNCFALSVKASGPTISRVHFGAGRHLDSRETFCLELLEHYAAAR
RMLGAPLQKRVRLQELCRQRIYAAVGRNLARIPLNVLRLDYLSSPFOI"
BASE COUNT 180 a 419 c 339 g 255 t
ORIGIN
Query Match 90.5%; Score 1117.8; DB 12; Length 1193;
Best Local Similarity 97.3%; Pred. No. 3.1e-192;

Matches 1137: Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 56 TGGCGGCGCTGTGCGACCGGAGCGCGGCTGACGCTGTGTCTCTCCCATACAGGAG 115
Db 25 TGGCGGAGACCGCGCGCGGAGCGCGGCTGACGCTGTGTCTCTCCCATACAGGAG 84
OY 116 CCGCGGAGCTATGAGCGCGCGGAGCGCGGCTGACGCTGTGTCTCTCCCATACAGGAG 175
Db 85 CCGCGGAGCTATGAGCGCGCGGAGCGCGGCTGACGCTGTGTCTCTCCCATACAGGAG 144
OY 176 CAGGTGGACCGCGACAAATGCGATCTCCCGGAGAGAGCCCGGAGCGGTCAAGGCC 235
Db 145 CAGGTGGACCGCGACAAATGCGATCTCCCGGAGAGAGCCCGGAGCGGTCAAGGCC 204
OY 236 TCCCTGCTGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 295
Db 205 TCCCTGCTGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
OY 296 GTCCAGGCGCGAGCGCGCTGCGGACATCTGCGACCTTCCGCTCCACTCCGATTAC 355
Db 265 GTCCAGGCGCGAGCGCGCTGCGGACATCTGCGACCTTCCGCTCCACTCCGATTAC 324
OY 356 CCGCGCATCAGCGGAGCAGCGCGCTCCTGAGAGCGCTGCGGCTTCTATTGGGAGCCCTG 415
Db 325 CCGCGCATCAGCGGAGCAGCGCGCTCCTGAGAGCGCTGCGGCTTCTATTGGGAGCCCTG 384
OY 416 AGCGTCAGCGGAGCAGCGAGCGGCTGCGGAGCGCGGCTGCGGAGCGGCTTCTGTCGC 475
Db 385 AGCGTCAGCGGAGCAGCGAGCGGCTGCGGAGCGCGGCTGCGGAGCGGCTTCTGTCGC 444
OY 476 GACAGCTGTCAACGAGACTGCTTCTGCGGCTCAGCGCTGAAGAGTGTGGGCGCCACG 535
Db 445 GACAGCTGTCAACGAGACTGCTTCTGCGGCTCAGCGCTGAAGAGTGTGGGCGCCACG 504
OY 536 AGCATCCGCGGAGCTTCCAGGCGCGGCGGCTTCCAGCTGAGCGGAGCGGAGAGCTTC 595
Db 505 AGCATCCGCGGAGCTTCCAGGCGCGGCGGCTTCCAGCTGAGCGGAGCGGAGAGCTTC 564
OY 596 GACTGCTTTTCGAGCTCTGTGAGCACTAGTGTGGGCGCGCGGCTGAGTGTGGGCGC 655
Db 565 GACTGCTTTTCGAGCTCTGTGAGCACTAGTGTGGGCGCGCGGCTGAGTGTGGGCGC 624
OY 656 CCGCTGCGCAGCGCGCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGC 715
Db 625 CCGCTGCGCAGCGCGCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGC 684
OY 716 GCGGTGGTGGGAGCACTGGCGGAGCTCCCTTACCGGCTGAGTCTCGTACACTG 775
Db 685 GCGGTGGTGGGAGCACTGGCGGAGCTCCCTTACCGGCTGAGTCTCGTACACTG 744
OY 776 AGTTCCTTCCCTTCAGATCTGACCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGC 835
Db 745 AGTTCCTTCCCTTCAGATCTGACCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGC 804
OY 836 CCTTATTTATTTCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 895
Db 805 CCTTATTTATTTCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 864
OY 896 CCGGTGGTGGGAGGAGTGTGTGAGGAGTGTGTGAGGAGTGTGTGAGGAGTGTGTGAGGAG 955
Db 865 CCGGTGGTGGGAGGAGTGTGTGAGGAGTGTGTGAGGAGTGTGTGAGGAGTGTGTGAGGAG 924
OY 956 CTCATCCCACTCTCAAGGGGTGGGGTGTCTCCCTTCCTGCTGCTCCTCCGGGTCCCCC 1015
Db 925 CTCATCCCACTCTCAAGGGGTGGGGTGTCTCCCTTCCTGCTGCTCCTCCGGGTCCCCC 984
OY 1016 TGGTGTGACAGCTGTGTCTGGGGCAGAGCACTGAATTCACCTCCTACCTCCATGTT 1075
Db 985 TGGTGTGACAGCTGTGTCTGGGGCAGAGCACTGAATTCACCTCCTACCTCCATGTT 1044
OY 1076 TACATATTCAGATATCTTTGCAACAACCGAGGGTGGGGAGGCTCTGAGCTCATTTT 1135
Db 1045 TACATATTCAGATATCTTTGCAACAACCGAGGGTGGGGAGGCTCTGAGCTCATTTT 1104

QY 1136 TCCTCTGCAGATATATCTATTTATTTTACAGCCAGTTAGGAATTAACCTTAT 1195
 Db 1105 TCCTCTGCAGATATATCTATTTATTTTACAGCCAGTTAGGAATTAACCTTAT 1164
 QY 1196 TATGAAGTTTTTTTTTAAAAAGAAAAA 1224
 Db 1165 TATGAAGTTTTTTTTTAAAAAGAAAAA 1193
 RESULT 4
 AF180302 1177 bp mRNA ROD 06-SEP-1999
 LOCUS AF180302 complete cds.
 DEFINITION AF180302.1 GI:5825619
 ACCESSION AF180302.1 GI:5825619
 VERSION AF180302.1
 KEYWORDS complete cds.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1177)
 Gregoroff, A., Pyronnet, S., Sonnenberg, N. and Veillette, A.
 Regulation of suppressor of cytokine signalling-1 (SOCS-1)
 expression by translational repression
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1177)
 Gregoroff, A., Pyronnet, S., Sonnenberg, N. and Veillette, A.
 Direct Submission
 Submitted (24-AUG-1999) McGill Cancer Centre, McGill University,
 3655 Drummond Street, Montreal, Quebec H3G 1V6, Canada
 JOURNAL
 TITLE
 FEATURES
 source location/Qualifiers
 1. 1177
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /chromosome="16"
 1. 1177
 /gene="SOCS1"
 /gene="SOCS1"
 /note="SOCS-1"
 /codon_start=1
 /product="suppressor of cytokine signalling-1"
 /protein_id="F4D53324.1"
 /db_xref="GI:5825620"
 /translation="MVARNQVADNMAISPAEPRRSEPSSSSSPPAAYPRPCP
 AVPAAPGDIHFRTFSRSHDYRITRISALDAGYWGFLSYGHERLRAPVCTF
 LVDSRORCFALSYKMASGPTSRVHROAGFHDGSRERDCLFELLEHYVAAPR
 RMLGAPLRORRVAPLOELCRORIVAVGRENARIPPLNPLNDYLSPPFQI"
 BASE COUNT 171 a 420 c 340 g 246 t
 ORIGIN
 Query Match 88.9%; Score 1098.4; DB 12; Length 1177;
 Best local Similarity 97.3%; Pred. No. 9.8e-189;
 Matches 1117; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 296 GTCCACAGCCAGCCCTGGGAGACACTCTCCGACACTTCCGACCTCCGACTCCGATTAC 355
 Db 270 GTCCACAGCCAGCCCTGGGAGACACTCTCCGACACTTCCGACTCCGACTCCGATTAC 329
 QY 356 CGGCGCATACAGCGGAGACAGCGGCTCTTGAGACGCTTGCGGCTTCTATTGGGACCCCTG 415
 Db 330 CGGCGCATACAGCGGAGACAGCGGCTCTTGAGAGCCCTGCGGCTTCTATTGGGACCCCTG 389
 QY 416 AGCGTCAGCGGGGCGACAGACGCGCTCGTCGCGAGCCCGTGGACCTTCTTGTCGCGC 475
 Db 390 AGCGTCAGCGGGGCGACAGACGCGCTCGTCGCGAGCCCGTGGACACTTCTTGTCGCGC 449
 QY 476 GACAGTGTAAAGGAACTCTTCTTGCGCTAGCGCTGAAGATGGCTTGGGCGCCACG 535
 Db 450 GACAGTGTAAAGGAACTCTTCTTGCGCTAGCGCTGAAGATGGCTTGGGCGCCACG 509
 QY 536 AGCATCCGCTGCACTTCCAGAGCGCGGCTTCCACTTGGACGACCGGAGACCTTC 595
 Db 510 AGCATCCGCTGCACTTCCAGAGCGCGGCTTCCACTTGGACGACCGGAGACCTTC 569
 QY 596 GACTGCCCTTTCAGCTGCTGAGACACTACGTGAGCGCGCGCGCATGTTGGGGCC 655
 Db 570 GACTGCCCTTTCAGCTGCTGAGACACTACGTGAGCGCGCGCGCATGTTGGGGCC 629
 QY 656 CCGCTGGCGAGCGCGGCTGCGGCGCTGAGAGCTGTGCGCAGCGCATGTGGCC 715
 Db 630 CCGCTGGCGAGCGCGGCTGCGGCGCTGAGAGCTGTGCGCAGCGCATGTGGCC 689
 QY 716 GCGTGGGTGCGAGAACTGCGCGCATCCCTTTAACCCGCTACTCCGTAACCTG 775
 Db 690 GCGTGGGTGCGAGAACTGCGCGCATCCCTTTAACCCGCTACTCCGTAACCTG 749
 QY 776 AGTTCTTCCCTTCAGACTGACCGCGCTGCGCTGCGCGACGATTAGTGGGGCG 835
 Db 750 AGTTCTTCCCTTCAGACTGACCGCGCTGCGCTGCGCGACGATTAGTGGGGCG 809
 QY 836 CCTATTATTCTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 895
 Db 810 CCTATTATTCTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 869
 QY 896 CGCCTGGGTGAGAGGAGTGTGAGAGGTGAGATCCCTCCACTTGTGCTGAGAC 955
 Db 870 CGCCTGGGTGAGAGGAGTGTGAGAGGTGAGATCCCTCCACTTGTGCTGAGAC 929
 QY 956 CTATCCCACTCTCAGGGGTGGGGGTGCTCCCTCTGCTGCTCCCTCGGGTCCCCC 1015
 Db 930 CTATCCCACTCTCAGGGGTGGGGGTGCTCCCTCTGCTGCTCCCTCGGGTCCCCC 989
 QY 1016 TGGTGTAGCAGCTGTGCTGGGGGCGAGACCTGAATTCACCTCACTCACTCACTGT 1075
 Db 990 TGGTGTAGCAGCTGTGCTGGGGGCGAGACCTGAATTCACCTCACTCACTCACTGT 1049
 QY 1076 TACATATTCAGATCTTTCACAAACAGGGGTGCGGAGGGTCTGAGCTTCATTT 1135
 Db 1050 TACATATTCAGATCTTTCACAAACAGGGGTGCGGAGGGTCTGAGCTTCATTT 1109
 QY 1136 TCCTCTGCAGATATATCTATTTTATTTTACAGCCAGTTAGGAATTAACCTTAT 1195
 Db 1110 TCCTCTGCAGATATATCTATTTTATTTTACAGCCAGTTAGGAATTAACCTTAT 1169
 QY 1196 TATGAAG 1203
 Db 1170 TATGAAG 1177
 RESULT 5
 BTPTMTNP2 13187 bp DNA ROD 11-DEC-1996
 LOCUS BTPTMTNP2 R.norvegicus PRM1, PRM2, PRM3 and TNP2 genes.
 DEFINITION 246939.1 GI:1359527
 ACCESSION 246939.1 GI:1359527
 VERSION
 KEYWORDS PRM1 gene; PRM2 gene; PRM3 gene; protamine; TNP2 gene; transition

```

SOURCE          protein 2.  
                Norway rat.  
ORGANISM        Rattus norvegicus  
REFERENCE       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
AUTHORS         Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
TITLE           1 (bases 1 to 13187)  
                Schluter,G., Celik,A., Obata,F., Schlicker,M., Hofferbert,S.,  
                Schlung,A., Adam,I.M. and Engel,W.  
                Sequence analysis of the conserved protamine gene cluster shows  
                that it contains a fourth expressed gene  
JOURNAL         Mol. Reprod. Dev. 43 (1), 1-6 (1996)  
MEDLINE         96341725  
REFERENCE       2 (bases 1 to 13187)  
AUTHORS         Schluter,G.  
TITLE           Direct Submission  
JOURNAL         Submitted (16-DEC-1994) schluter G., Institut fuer Humangenetik,  
                Universitaet Goettingen, Goslarstr. 12d, Goettingen, FGR, 37073  
REMARK          Revised by [3]  
REFERENCE       3 (bases 1 to 13187)  
AUTHORS         Schluter,G.  
TITLE           Direct Submission  
JOURNAL         Submitted (30-MAY-1996) schluter G., Institut fuer Humangenetik,  
                Universitaet Goettingen, Goslarstr. 12d, Goettingen, FGR, 37073  
                4 (bases 1 to 13187)  
                Schluter,G., Celik,A., Obata,R., Schlicker,M., Hofferbert,S.,  
                Schlung,A., Adam,I.M. and Engel,W.  
                Sequence analysis of the conserved protamine gene cluster shows  
                that it contains a fourth expressed gene  
                unpublished  
JOURNAL         On Jun 5, 1996 this sequence version replaced g1:86653.  
COMMENT         Location/Qualifiers  
FEATURES        1..13187  
                 /organism="Rattus norvegicus"  
                 /db_xref="taxon:10116"  
                 /chromosome="10"  
gene            829..1075  
CDS             join(829..934,1026..1075)  
                /gene="PRM1"  
                /note="haploid expressed, male germcell specific,  
                chromatin binding"  
                /codon_start=1  
                /product="protamine 1"  
                /protein_id="CAAB7061.1"  
                /db_xref="GI:1359528"  
                /db_xref="SWISS-PROT:P10118"  
                /translation="MARYRCRSKSRCKRRRRRCRRRRRCRRRRRCRRRRRCRRRRRY"  
                TRICKRY"  
                1800..1860  
repeat_unit    /note="ID element"  
                complement(2270..2330)  
repeat_unit    /note="ID element"  
                complement(2405..2560)  
repeat_unit    /note="B2 element"  
                5326..5760  
gene            /gene="PRM2"  
CDS             join(5326..5586,5695..5760)  
                /gene="PRM2"  
                /note="haploid expressed, male germcell specific,  
                chromatin binding"  
                /codon_start=1  
                /product="protamine 2"  
                /protein_id="CAAB7062.1"  
                /db_xref="GI:1359529"  
                /db_xref="SWISS-PROT:P11248"  
                /translation="WVRYRMSPSGHQGPGDHEEEQGGELSPERYDGRTET  
                RGHHHRRCRLRIHKKRRSCRRRHSSCRHRRRRRVSTGCRRSRRCRCRCR  
                CRMYY"  
gene            6513..6827  
                /gene="PRM3"  
CDS             6513..6827  
                /gene="PRM3"  
                /note="haploid expressed, male germcell specific"

```

Query Match	Best Local Similarity	Score	DB 12:	Length
Matches 1160;	Conservative	0;	Mismatches 60;	Indels 8; Gaps 3;
QY 1	CGAGGCTAAGCTCGGGGCGATTTCGGGTGCGCTCCGCTCTTGGGGTCTGTGGCC	60		
DB 11959	CGAGGCTAAGCTCGGGGCGATTTCGGGTGCGCTCCGCTCTTGGGGTCTGTGGCC	12018		
QY 61	GACCTGTGCCAACCAGGCGCCGGCTACTGCTCTCTCTCCCATAGAGGACCCG	120		
DB 12019	GACCTGTGCCAACCAGGCGCCGGCTACTGCTCTCTCTCCCATAGAGGACCCG	12078		
QY 121	GACGTTATGGCCACCCCTCCAGCTGGCCCTCGAGTATGATGTTAGCAGCAACAGT	180		
DB 12079	GACGTTATGGCCACCCCTCCAGCTGGCCCTCGAGTATGATGTTAGCAGCAACAGT	12138		
QY 181	GACAGCCAGATGATGATCTCCCGGCGAGAGAGCCCGAGGCGGTGAGAGCCCTCTC	240		
DB 12139	GAGAGCCAGATGATGATCTCCCGGCGAGAGAGCCCGAGGCGGTGAGAGCCCTCTC	12198		
QY 241	GTCCTGTCTTCTGTCCTGCGAGCGGCGCCGCTGCTCCCGGCTGCGCGGGTCC	300		
DB 12199	GTCCTGTCTTCTGTCCTGCGAGCGGCGCCGCTGCTCCCGGCTGCGCGGGTCC	12258		
QY 301	AGCCCGACCCCTGGCGAGCATCACTTCGGAGCTCCGCTCCGATCCGATTACGGCG	360		
DB 12259	AGCCCGACCCCTGGCGAGCATCACTTCGGAGCTCCGCTCCGATCCGATTACGGCG	12318		
QY 361	CATCAGCGGAGCAGCGGCTCTGAGAGCCCTGGGCTTCTATTGGGAGCCCTGAGCGT	420		
DB 12319	CATCAGCGGAGCAGCGGCTCTGAGAGCCCTGGGCTTCTATTGGGAGCCCTGAGCGT	12378		
QY 421	GCAGCGGGCGCAGAGCGGCTGCGTGGAGCCGCTGGGACACTTCTTGGTGGCGAGAG	480		
DB 12379	GCATGGGGCGCAGAGCGGCTGCGTGGAGCCGCTGGGACACTTCTTGGTGGCGAGAG	12438		
QY 481	TGCTTAAGGGAAGTCTTCTCGGGCTAGAGGTGAATGGCTTCGGGCGCCAGAGAGAT	540		
DB 12439	TGCTTAAGGGAAGTCTTCTCGGGCTAGAGGTGAATGGCTTCGGGCGCCAGAGAGAT	12498		
QY 541	CCGCGTGCACTTCAGGCGCGCTTCGACTTGAAGGCGAGCGCGAGACCTTCGACTG	600		
DB 12499	TCGCTGCACTTCAGGCGCGCTTCGACTTGAAGGCGAGCGCGAGACCTTCGACTG	12558		
QY 601	CCCTTTTCAGAGTGTGAGAGCACTACGTGGCGGCGCGCGCGGATGTTGGGGGCGCGCT	660		
DB 12559	CCCTTTTCAGAGTGTGAGAGCACTACGTGGCGGCGCGCGCGGATGTTGGGGGCGCGCT	12618		

DB	781	CTCTGCGGAGAGACCTCATCCACCTCCAGGAGGCGGGGCTCCTCCCTCGGTGCTC	840
QY	1001	CCTCGGGGTCCTCCGCTGTTGTAGACGCTTGTGTCTGGGGCCAGGACCTGAAATTCACATC	1060
DB	841	CTCCGGGCCCCCGGTTGAGACGCTGTCTGGGGCCAGGACCTGAAATTCACATC	900
QY	1061	CTACCTCTCATGTTTACATATCCAGTATCTTTCACAAACACAGGGGTCGGGAGGCT	1120
DB	901	CTACCTCTCATGTTTACATATCCAGTATCTTTCACAAACACAGGGGTCGGGAGGCT	960
QY	1121	CTCTGCGCTCATATTTTCTGCTGTGCAAAATCCATATTTATATTTTACAGCCAGTTTA	1180
DB	961	CTCTGCGCTCATATTTTCTGCTGTGCAAAATCCATATTTATATTTTACAGCCAGTTTA	1020
QY	1181	GGTAATAACCTTATATGAAAGTTTATTTTAAAA	1216
DB	1021	GGTAATAACCTTATATGAAAGTTTATTTTAAAA	1056
RESULT	7		
AB000710	909 bp	MRNA	ROD 22-JUL-1997
LOCUS			
DEFINITION	Mus musculus mRNA for stat-induced stat inhibitor-1, complete cds.		
ACCESSION	AB000710.1	GI:2274773	
VERSION	stat-induced stat inhibitor-1; SSI-1.		
KEYWORDS	Mus musculus cDNA to mRNA, clone, lib:thymus cDNA.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 909)		
AUTHORS	Kishimoto, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-Jan-1997) to the DDBJ/EMBL/Genbank databases.		
REFERENCE	2-2, Saita 565, Japan (E-mail: matsumoto@med3.med.osaka-u.ac.jp, Tel: +81-6-879-3831, Fax: +81-6-879-3839)		
AUTHORS	2 (bases 1 to 909)		
TITLE	Naka, T., Narazaki, M., Hirata, M., Tomoshige, M., Minamoto, S., Nishimoto, N., Kajita, T., Yoshizaki, K., Akira, S. and Kishimoto, T.		
JOURNAL	Structure and function of a novel STATs-induced inhibitor of STATs function-1 (SIIS-1)		
REFERENCE	3 (sites)		
AUTHORS	Naka, T., Narazaki, M., Hirata, M., Matsumoto, T., Minamoto, S., Aono, A., Nishimoto, N., Kajita, T., Taga, T., Yoshizaki, K., Akira, S. and Kishimoto, T.		
TITLE	Structure and function of a new STAT-induced STAT inhibitor		
JOURNAL	Nature 387 (6636), 924-929 (1997)		
MEDLINE	97345635		
FEATURES			
Source	Location/Qualifiers		
gene	1..909		
CDS	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
	/clone_lib="thymus CDNA"		
	55..693		
	/gene="SSI-1"		
	55..693		
	/gene="SSI-1"		
	/codon_start=1		
	/product="stat-induced stat inhibitor-1"		
	/protein_id="BA021539.1"		
	/db_xref="GI:2274774"		
	/translation="MARNQVAADNIAISPAAPRRSPSSSSSSSPAAPRRPCTGVPAPAPDTHFRTRFSDDYRRITRTSALIDACGFTGVP/SVGAHRRLEAPVGTGLVDRSDRQFALSVKMASTPSTIRVFQAGREHLDNRSTFDCLFELSHYVAAPRMLGAPLQRRVRRPQELCRQRIYAAVGRNRLARIPLVLDYLSPPFOI"		
BASE COUNT	121 a 338 c 274 g 176 t		
ORIGIN			

Best Local Similarity 99.7%; Pred. No. 9.4e-154;
Matches 906; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	107	TCGGCGCACCCCGAGCGGTATGAGCCACCCCTCCAGCTGAGGCCCCCTCGAGTGAAGTGA	166
Db	1	TCAGCGACGACCCCGAGCGGTATGAGCCACCCCTCCAGCTGAGGCCCCCTCGAGTGAAGTGA	60
QY	167	GCACGCAACAGGTGGCAGCCGACATGCGATCTCCCGCGCAGCAGAGCCCGACGCGG	226
Db	61	GCACGCAACAGGTGGCAGCCGACATGCGATCTCCCGCGCAGCAGAGCCCGACGCGG	120
QY	227	TCAGAGCCCTCTCGTCTCTGCTTGTGTCTGTGCGCAGCGGCCCCGTGCTCCCCGGCCC	286
Db	121	TCAGAGCCCTCTCGTCTCTGCTTGTGTCTGTGCGCAGCGGCCCCGTGCTCCCCGGCCC	180
QY	287	TGCGCGGCGGTGCCAGCGCCCGACGCGCTGGCGACACACTTCGCGACTTTCGCTCCAC	346
Db	181	TGCGCGGCGGTGCCAGCGCCCGACGCGCTGGCGACACACTTCGCGACTTTCGCTCCAC	240
QY	347	TCCGATTACCGGCGCATCAGCGCGACAGCGCGCTCTGGAGCGCTGCGGCTTATTGG	406
Db	241	TCCGATTACCGGCGCATCAGCGCGACAGCGCGCTCTGGAGCGCTGCGGCTTATTGG	300
QY	407	GCACCCCTAAGGTGCGACGCGGCGCAGCAGCGCGCTGCGGCGAGCCCTGGGCGACTTC	466
Db	301	GCACCCCTAAGGTGCGACGCGGCGCAGCAGCGCGCTGCGGCGAGCCCTGGGCGACTTC	360
QY	467	TTGGTGCAGGAGTGTGTCAAGGAACTCTTCTTGCAGCTCAGCGGTGAAGATGGCTTCG	526
Db	361	TTGGTGCAGGAGTGTGTCAAGGAACTCTTCTTGCAGCTCAGCGGTGAAGATGGCTTCG	420
QY	527	GGCCCCAGAGCATCGCGCTGCATCTTCCAGGCGCGGCGGCTTCACCTTGGAGCGACGCG	586
Db	421	GGCCCCAGAGCATCGCGCTGCATCTTCCAGGCGCGGCGGCTTCACCTTGGAGCGACCGC	480
QY	587	GAGACCTTCGATGCTCTTTGAGGTGCGAGAGCACTACGTGGCGGCGCGCGCGCAGT	646
Db	481	GAGACCTTCGATGCTCTTTGAGGTGCGAGAGCACTACGTGGCGGCGCGCGCGCAGT	540
QY	647	TTGGGGGGCCCCGCTGCGCAGCGCGCGCGCTGCGCAGAGACTGTGTCCAGCGC	706
Db	541	TTGGGGGGCCCCGCTGCGCAGCGCGCGCGCTGCGCAGAGACTGTGTCCAGCGC	600
QY	707	ATCGTGTGCGCGCGGTGGGTGCGAGAACTGCGCGCGATCCCTTAACCGGTACTCGT	766
Db	601	ATCGTGTGCGCGCGGTGGGTGCGAGAACTGCGCGCGATCCCTTAACCGGTACTCGT	660
QY	767	GACTACGTAGTTCCTTCCCTTCCAGATCTACCGGGCTGCGGCTGCGCGAGATTAA	826
Db	661	GACTACGTAGTTCCTTCCCTTCCAGATCTACCGGGCTGCGGCTGCGCGAGATTAA	720
QY	827	GTGGGGGGCGCTTATTATTCTTATTATTATTATTATTATTCTTCTGGAACAGGTGG	886
Db	721	GTGGGGGGCGCTTATTATTCTTATTATTATTATTATTATTCTTCTGGAACAGGTGG	780
QY	887	AGCCCTCCCGCGCTGGGTGGAAGGAGTGTGTGAGAGGTGAGATGCTCCCACTTCG	946
Db	781	AGCCCTCCCGCGCTGGGTGGAAGGAGTGTGTGAGAGGTGAGATGCTCCCACTTCG	840
QY	947	GCTGAGAGACTATCCCACTCTCAGAGGGGTGGGGGTGCGCCCTCGTGGTGTCCCTCG	1006
Db	841	GCTGAGAGACTATCCCACTCTCAGAGGGGTGGGGGTGCGCCCTCGTGGTGTCCCTCG	900
QY	1007	GGTCCCGCC 1015	
Db	901	GGTCCCGCC 909	
RESULT	8		
AC002286	12599 bp	DNA	PR1 23-NOV-1999
LOCUS	AC002286		
DEFINITION	Homo sapiens Chromosome 16p13.13 cosmid clone 35667 from the Losb		
	Almos Chromosome 16 Specific Superfos cosmid library complete		

genomic sequence, complete sequence.

AC002286
VERSION AC002286.1 GI:2160310
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 12589)
TITLE Kramer, J.A., Adams, M.D., Singh, G.B., Doggett, N.A. and Krawetz, S.A. Extended analysis of the region encompassing the PRM1-2PRM2-2TNP2 domain: genomic organization, evolution and gene identification
J. Exp. Zool. 282 (1-2), 245-253 (1998)
98390623

JOURNAL MEDLINE
REFERENCE 2 (bases 1 to 12589)
AUTHORS Loftus, B.J., Kim, U.J., Sneddon, V.P., Kalush, F., Brandon, R., Fuhrmann, J., Mason, T., Crosby, M.L., Barnstead, M., Cronin, L., Deslattes Mays, A., Cao, Y., Xu, R.X., Kang, H.L., Mitchell, S., Eichler, E.E., Harris, P.C., Venter, J.C. and Adams, M.D.
Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q
Genomics 60 (3), 295-308 (1999)

TITLE 3 (bases 1 to 12589)
JOURNAL MEDLINE
REFERENCE 3 (bases 1 to 12589)
AUTHORS Adams, M.D.
Direct Submission
Submitted (04-JUN-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
4 (bases 1 to 12589)
Adams, M.D., Loftus, B.J., Zhou, L., La Bombard, M., Kim, U.J., Venter, J.C., Kramer, J.A. and Doggett, N.A.
Direct Submission
Submitted (28-AUG-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
Address all correspondence to:
Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr.,
Rockville, MD 20850,
USA e-mail address: mdadams@tigr.org. The cosmid location is on chromosome 16p13.13. The orientation of the sequence is from SP6 end to 3' end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), GeneFinder (Phil Green, University of Washington), Genscan (Chris Burge, <http://genomic.stanford.edu/~chris/GENSCANW.html>) searches of the complete sequence against a peptide database, and the EST database at TIGR (<http://www.tigr.org/cdb/at.html>). A gene with homology to another protein is annotated as the isolog of that protein. Genes without peptide homology having spliced EST hits are termed 'unknown protein'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).

FEATURES
source Location/Qualifiers
1..12589
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/map="16"
/clone="Protlam16"
repeat_region complement(381..440)
/rpt_family="GC-rich"
repeat_region complement(751..806)
/rpt_family="GC-rich"
repeat_region complement(1318..1361)
/rpt_family="AT-rich"
repeat_region complement(1572..1700)
/rpt_family="MIR"
repeat_region complement(2627..2730)
/rpt_family="(GAAA)n"
repeat_region complement(2846..2888)
/rpt_family="MIR"
repeat_region complement(3026..3134)
/rpt_family="MIR"

repeat_region complement(3458..3501)
/rpt_family="(CA)n"
repeat_region complement(3810..3902)
/rpt_family="MIR"
repeat_region complement(3936..4240)
/rpt_family="AluIo"
repeat_region complement(4318..4367)
/rpt_family="MIR"
repeat_region 4394..4455
/rpt_family="MIR"
repeat_region complement(4569..4864)
/rpt_family="AluIo"
repeat_region 6540..6617
/rpt_family="MIR"
repeat_region complement(6655..6705)
/rpt_family="(GAA)n"
repeat_region 6726..7025
/rpt_family="Alusx"
repeat_region complement(7029..7296)
/rpt_family="AluIo"
repeat_region complement(7445..7614)
/rpt_family="MIR"
repeat_region 8005..8310
/rpt_family="Alusx"
repeat_region 8311..8358
/rpt_family="(GAAA)n"
repeat_region 8359..8659
/rpt_family="Alusx"
repeat_region 8938..9009
/rpt_family="MIR"
repeat_region 9021..9331
/rpt_family="AluIo"
repeat_region complement(9842..9998)
/rpt_family="MIR"
repeat_region 10416..10552
/rpt_family="MIR"
repeat_region 10557..10599
/rpt_family="POLY_A"
repeat_region 10682..10889
/rpt_family="Alusx"
repeat_region complement(11234..11542)
/rpt_family="AluY"
repeat_region 12198..12309
/rpt_family="(CAT)n"
misc_feature complement(12203..12589)
/note="has high homology to Human nuclear ribonucleoprotein particle (hnRNP) C protein"
evidence=not-experimental

BASE COUNT 3067 a 3233 c 3521 g 3068 t
ORIGIN

Query Match 58.8%; Score 725.6; DB 40; Length 12589;
Best Local Similarity 80.7%; Pred. No. 1.3e-121;
Matches 1004; Conservative 0; Mismatches 204; Indels 36; Gaps 12;

QY 6 CTCAGCTCCGCGCGGATTCCTGCGGCTCTGCTCTCTGCGGCTGCTGCGGCGCT 65
DB 131 CCTAGGGGCGGGGCTCCGCCGGGAGCGCGCTCGGAGTTCTCCGGCGGCGCACACT 190
QY 66 GTGCCACCGGAGCGCGGCTCATGCTCTCTC-CCCATCAGCGAGCGCGGAGC 124
DB 191 GCCCGGCGCGGAGCGCGGCTCATGCTCTCTCTCTCCGCGAGCGAGCGCGGAGC 250
QY 135 CTATGGCCACCGCTTCACAGCTGCGGCTCTGAGTAGAGTAGACGACGACAGGTGCA 184
DB 251 CTATGGCCACCGCTTCACAGCTGCGGCTCTGAGTAGAGTAGACGACGACAGGTGCA 310
QY 165 GCGGCAATGGAGTCTCCCGGCGAGAGCGCGGCGGCTGAGAGCGGCTGCTGCTCC 244
DB 311 GCGGCAATGGAGTCTCCAGACAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 367
QY 245 TCGTCTGCTCTCCAGCGCGCGCGGCTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCG 304

Db	368	TTCTTCTCTCTCTCTGCGCGGGGGCCCCCGCGGGCCCGGGGGCGTCCCGCGGGCTCCGGCC	427
Oy	305	CCAGCCCTTGGCGACACTTCTCCGACACTTCGCGCTCCCACTCCGATTACCGGCGATC	364
Db	428	CCGGCCCCCGGGGACACGACACTTCGCGACATTCCGTTCTGCAAGCGCGATTACCGCGCATC	487
Oy	365	ACGGGACAGGGCGCTCTTGAGACGCTCGGGGCTTCTATTGGGGAACCGCTAGGCTCAC	424
Db	488	ACGCGCGCCAGCGCGCTCTTGAGACGCTCTGAGACGCTCTGCGGATTTCTACTGGGGGCCCTTACGCTCAC	547
Oy	425	GGGGCGCACGAGCGGCTCGTGGCGAGCCGCTGGGCGACCTTCTTGTCGCGACATGCT	484
Db	548	GGGGCGCACGAGCGGCTCGCGCGCGAGCGCGCTGGGCGACCTTCTGTCGGCGACAGCGCG	607
Oy	485	CAACGGAATCTGTTCTTGGCGCTCAGGCTGAAAGATGGCTTGGGGGCCACGAGCATCGC	544
Db	608	CAGCGGAATCTGTTTGGCCCTTAGCTGAAGATGGCTCTGGGACCCAGACGATCGC	667
Oy	545	GTGCACTTCAGAGCGCGCGCTTCCACTTGGAGCGGACCGCGAGACCTTGCATGCTT	604
Db	668	GTGCACTTCAGAGCGCGCGCTTTCACCTGGATGGAGCGCGGAGAGCTTGATGCTCTC	727
Oy	605	TTGCACTGCTGGAGCACTACGTGGCGGCGCGCGCGCATGTTGGGGGCCCGGCTCGC	664
Db	728	TTGCACTGCTGGAGCACTACGTGGCGGCGCGCGCGCATGCTGGGGGCCCGGCTCGC	787
Oy	665	CAGCGCGCGCGCGCGCTCGAGAGAGCTGTGTGCGCGACATCGTGGCGCGCGTGGT	724
Db	788	CAGCGCGCGCGCGCGCGCTCGAGAGAGCTGTGTGCGCGACATCGTGGCGCGCGTGGT	847
Oy	725	CGCGAAGACTGGCGGCGCATCCCTCTTAAACCGGCTACTCGGTGACTAGTTCCTTC	784
Db	848	CGCGAAGACTGGCGGCGCATCCCTCTTAAACCGGCTACTCGGTGACTAGTTCCTTC	907
Oy	785	CCCTCCAGATCTGACCGGCGTGGCGGCTGTGGCGAGCATTAAGTGGGGGGCGCTATTAT	844
Db	908	CCCTCCAGATTTTGACCGGCGAGCGCGCGCTGTGACGAGCATTAACGTGGATGCCGTGT	967
Oy	845	TTCTATTATTATTATTATTATTATTATTCTGGAACACAGGTGGAGCCCTCCCGC-GCCTGGG	903
Db	968	TATT-----TTGTATTACTTGCTGTGAACCATGTGGGTACCTCCCGGCGCTGGG	1018
Oy	904	TCGAGGAGAGTGTGTG---GAGGGTAAATGCTCTCCCACTTGTGGCTGAGA-----C	955
Db	1019	TTGGAGGAGAGGAGGTGTGAGGGGCGAGCGGCTCCCGGCTCGGCTGGAGACGAGGC	1078
Oy	956	CTCATCCCACTCTCAGGGGTGGGGGTGCT----CCCTCTGTGTGCTCCCTCCGAGTCC	1011
Db	1079	CGGAGACCCCTTCACTCTGTGAGGGGGTCTCCCTCTGTGTGCTCCCTCTGTGGTCC	1138
Oy	1012	CCC-CTGCTGTAGACACT---TGCTGTGGGGCCAGACCTGAATT--CCACTCTTA	1063
Db	1139	CCCTGCTGTGTGTAGACACTTACGTATCTGTGAGCGAGGACCTGAACCTGCACTCTTA	1198
Oy	1064	CCCTCCATGTTTCATATTCCTCCAGTATCTTGTGACAAACACAGGGG-TCGGGAGGGTCT	1122
Db	1199	CCCTCTCATGTGTACATATACCCAGTATCTTGTGACAAACACAGGGGTGGGGAGGGTCT	1258
Oy	1123	CTGGCTCATTTTCTGCTGTGCAAAATATCCTATTATATTATTTTTCAGCCAGTTAGG	1182
Db	1259	CTGGCTCATTTTCTGCTGTGCAAAATATCTTATTTAT-TTTTAAAGTCAAGTTAGG	1317
Oy	1183	TAAATAACTTTATATGAAATTTTTTTTTTAAAGAAAAAAA 1226	
Db	1318	TAAATAACTTTATATGAAAGTTTTTTTTTAAAAAAAATAA 1361	

Accession	AC002047
Version	AC002047.1 GI:2062143
KeyWords	HNG: HNGS_PHASE1.
Source	human.
Organism	Homo sapiens
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Title	1 (bases 1 to 25417)
Journal	Adams,M.D., Loftus,B.J., Zhou,L., Phillips,C., Brandon,R.C., Fuhrmann,J., Kim,U.J., Keilavage,A.R. and Venter,J.C. Human chromosome 16p13 BAC clone C1987SK-Protamine16 Unpublished
Reference Authors	2 (bases 1 to 25417)
Journal	Adams,M.D. and Loftus,B.J.
Reference Authors	Direct Submission
Journal	Submitted (29-APR-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
Reference Authors	3 (bases 1 to 25417)
Journal	Adams,M.D.
Reference Authors	Direct Submission
Journal	Submitted (30-APR-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
Comment	* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Features	FEATURES source
Base Count	BASE COUNT ORIGIN
Query Match	58.8%; Score 725.6; DB 32; Length 25417;
Best Local Similarity	80.7%; Pred. No. 1.2e-121;
Matches 1004:	Conservative 0; Mismatches 204; Indels 36; Gaps 12.
6 CTCAAGCTCCGGGCGGATTCGCGTTCGCTCCTTGCGGTCTGTGGCGGCCT	65
370 CCCCTAGGGCGGGGTCGCCGGGAGGGCGCCCTCGGAGTTGTCCGGCGGCACACT	429
66 GTGCCACCCGGAAGCGCGGCTCACAGCTCTGTCTC -CCCATTAGCGCAGCGCGGAG	124
430 GCCCGCCCCCGAGGCGCCCACTCACCGCTTGTCTCCCGCAGCGCAGCCCGGAG	489
125 CTATGGCCACCCTTCACAGCTGGCGCCCTTCGATGAGTAGATGTAGCAGCAACGAGTGGCA	184
430 CTATGGCCACCCTTCGCGGCTGGCCCTTCTGTAGATGATGTAGCAGCACAACGAGTGGCA	549
185 GCCGCAATGCGATTCCTCCCGGCGCAGCAAGCCCGCAGCGCGGTCTAGAGCCCTCTCTGTC	244
550 GCCGCAATGCAAGTCTCCACAGCAGCAGAAGCCCGCAGCGCGCTTCC---TTC	606
245 TCGTTTGTCTCGTCCGACAGCGCGCCGCTGGCGTCCCGGCGCTGCGCGGAGTCCAGCC	304
607 TCTTCTCTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGCCTCCCGGC	666
305 CCAGCCCTGCGGACACTTCCGACCTTCGCGCTCCCACTCCGATTACCGGCGCATC	364
667 CCGGCCCCCGGAGACGACACTTCGCGACATTCCGCTTCGACGCGGATTACCGGCGCATC	726
355 ACGGCGGACACGCGCTCTGAGAGCGCTGCGGCTTCTATTGGGAGACCCCTAGAGCTGCAC	424
727 ACGGCGGACACGCGCTCTGAGAGCGCTGCGGATTTACTGGGCGCGCTGAGCGCTGCAC	786

OY 492 ACTGCTCTGCGCTGACGCGTGAAGATGGCTTCGGGCCCCACAGACATCCGCGTCACT 551
 DB 483 ACTGCTTTTTCCTTACGCTGGAAGATGGCTTCGGGCCCCACAGACATCCGCGTCACT 542
 OY 552 TCCAGCGCGCGCGCTTCCACTTGAAGAGCGAGCGGAGACTTGCAGTCCCTTTTCGAGC 611
 DB 543 TTCAGCGCGCGCGCTTTCACCTGAGATGGAGCGGAGAGCTTGCAGTCCCTTTTCGAGC 602
 OY 612 TGTCTGAGACACTACATGAGCGCGCGCGCGCGCATGTGGGGCCCCGCTTCGCGCAGCGC 671
 DB 603 TGTCTGAGACACTACATGAGCGCGCGCGCGCGCATGTGGGGCCCCGCTTCGCGCAGCGC 662
 OY 672 GCGTGGCGCGCGCTGAGAGAGCTGTGTCGCGAGCATGCTGGCGCGCGCGCGCGAGAG 731
 DB 663 GCGTGGCGCGCGCTGAGAGAGCTGTGTCGCGAGCATGCTGGCGCGCGCGCGCGAGAG 722
 OY 732 ACCGTGGCGCGCATCCCTCTTAAACCGGTAACCTGTAACCTGTAACCTGTAACCTGTAAC 791
 DB 723 ACCGTGGCGCGCATCCCTCTTAAACCGGTAACCTGTAACCTGTAACCTGTAACCTGTAAC 782
 OY 792 AGATCTGACCGCGCTCCGCTGTGCGCGAGCATTAAGTGGGGCGCGCTTCTTATTTCTTAT 851
 DB 783 AGATCTGACCGCGCGCTCCGCTGTGCGCGAGCATTAAGTGGGGCGCGCTTCTTATTTAT 840
 OY 852 TATTAATTAATTAATTAATTTTTCGGAACACAGTGGGAGCGCCCTCCCGC-GCCTGGTGGAGG 910
 DB 840 -----TGTATTACTTACTTCTGGAACCATGTGGGTACCTTCCCGCGCTGGGTTGGAGG 893
 OY 911 GAGTGGTGTG---GAGGAGTGAATGCTCCACATCTTGGCTGAGAG-----CCTCATCC 962
 DB 894 GAGCGGATGGGTGTAGGGGCGAGGCGCTCCCGCTCGGTGGAGAGAGCGCGAGAGC 953
 OY 963 CACCTCTACAGGAGGAGGAGGAGT-----CCCTCTGAGTGTCTCCCTCCGAGTCTCCCT 1016
 DB 954 CCCTCTACAGCTCTGAGGAGGAGGAGTCTCCCTCTGAGTGTCTCCCTCTGAGTCTCCCT 1013
 OY 1017 GGTGTAGAGAGCT---TGTGTCTGGGAGCGAGAGCTGAAAT--CCAGCTACAGCTCC 1070
 DB 1014 TGTGTAGAGAGCTTACGTGTATCTGAGAGCGAGAGCTGAACTCTCACTCTTTC 1073
 OY 1071 ATGTTACATATATCCAGATATCTTTCACAAACAGAGGAG--TCGGGAGAGGAGTCTGAGCT 1129
 DB 1074 ATGTTACATATATACAGATATCTTTCACAAACAGAGGAGTCTGAGGAGTCTGAGCT 1133
 OY 1130 CATTTTCTGCTGTCAGAGATATCTTATTTATTTATTTTACAGCAGTTCAGTAAATAA 1189
 DB 1134 TATTTTCTGCTGTCAGAGATATCTTATTTATTTTATTTTAAAGTCAAGTTAGTAAATAA 1192
 OY 1190 CTTTATTAAGAAAGTTTATTTT 1212
 DB 1193 CTTTATTAAGAAAGTTTATTTT 1215

RESULT 12
 HSU88326 1094 bp mRNA PRI 06-JUL-1997
 LOCUS Human suppressor of cytokine signalling-1 (SOCS-1) mRNA, complete cds.
 DEFINITION
 ACCESSION U88326 GI:2245383
 VERSION U88326.1
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 1094)
 Starr, R., Willison, T.A., Viney, E.M., Murray, L.J.L., Rayner, J.R.,
 Jenkins, B.J., Gonde, T.J., Alexander, W.S., Metcalf, D., Nicola, N.A.,
 and Hilton, D.J.
 TITLE A family of cytokine-inducible inhibitors of signalling
 JOURNAL Nature 387 (6636), 917-921 (1997)
 MEDLINE 97345633
 REFERENCE 2 (bases 1 to 1094)

AUTHORS Starr, R., Willison, T.A., Viney, E.M., Murray, L.J.L., Rayner, J.R.,
 Jenkins, B.J., Gonde, T.J., Alexander, W.S., Metcalf, D., Nicola, N.A.,
 and Hilton, D.J.
 TITLE Direct Submission
 JOURNAL Submitted (04-FEB-1997) Cancer Research Unit, The Walter and Eliza
 Hall Institute of Medical Research, PO Royal Melbourne Hospital,
 VIC 3050, Australia
 FEATURES
 SOURCE location/Qualifiers
 1..1094
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="B lymphocyte"
 /cell_line="Raji cell line"
 24..659
 /gene="SOCS-1"
 /gene="SOCS-1"
 24..659
 /gene="SOCS-1"
 /codon_start=1
 /product="suppressor of cytokine signalling-1"
 /protein_id="AA82401.1"
 /db_xref="gi:2245384"
 /translation="MVANQVADNAVSTAEPRRPSPSSSSSSPAAPRPAPCPA
 VPAPAPDTHFRTRSHADYKRTIRASALDAGCFYWGPIVSHAEHLRAEPVGT
 VRSRORNCFFALSVKMASTSTIRVHOFGRFLDGSRESFDLFEIERYVAPPR
 MLAGPLRORRVRVPEICRORIVATVRENLARIPLNPLRDYLSFPFQI"
 BASE COUNT 167 a 381 c 313 g 233 t
 ORIGIN
 Query Match 55.9%; Score 690.2; DB 10; Length 1094;
 Best Local Similarity 83.5%; Pred. No. 3,2e-115;
 Matches 924; Conservative 0; Mismatches 148; Indels 35; Gaps 11;
 OY 138 CTCAGCTGGGCGCTCGAGTGAAGATGTAGACAGCAGCAGCAGTGGCAGCCGCAATGCGA 197
 DB 1 CTCGGGCTGGGCGCTTGTAGAGTGTAGCAGCAGCAGCAGTGGCAGCCGCAATGCGAG 60
 OY 198 TCTCCGCGAGAGAGCGCGGAGGCGGTGAGAGCGCTCCGTCGTCGTCGTCGTCGTCGTC 257
 DB 61 TCTCCAGAGAGAGAGCGCGGAGGCGCGGAGGCGCGCAAGCTTC--TCTCTCTCTCTCTCT 117
 OY 258 GCGAGCGCGCGCGCTGGTGTGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 317
 DB 118 CG 177
 OY 318 ACACCTACCTCCGACCTTCGCTCCGCTCCGATTCAGCCGCGGAGTCACGCGGAGCAGCG 377
 DB 178 ACACGACCTCCGACATTCGCTTCGACAGCGGATTCAGCGCGGAGTCACGCGGAGCAGCG 237
 OY 378 CGCTCTGAGAGCGCGCGGCTTCTATTTGGGAGCCCGTAGAGGTGACAGGCGGAGCAGAGC 437
 DB 238 CGCTCTGAGAGCGCGCGGATTCAGCTTCTAGTGGGCGCGCTAGCGTGCAGGCGGAGCAGAGC 297
 OY 438 GCGTCTGAGAGCGCGCGGCTTCTATTTGGGAGCCCGTAGAGGTGACAGGCGGAGCAGAGC 497
 DB 298 GCGTCTGAGAGCGCGCGGCTTCTATTTGGGAGCCCGTAGAGGTGACAGGCGGAGCAGAGC 357
 OY 498 TCTTGGCGCTAGAGGTGAGATGCTTGGGCGCGCGAGAGATCCGCGTGCACCTTCAGG 557
 DB 358 TTTTGGCGCTTAGAGGTGAGATGCTTGGGCGCGCGAGAGATCCGCGTGCACCTTCAGG 417
 OY 558 CCGGCGCTTACATGAGAGGAGCGCGGAGAGCTTGCAGTCCCTTTCAGAGCTGCGG 617
 DB 418 CCGGCGCTTACATGAGATGAGAGCGCGGAGAGCTTGCAGTCCCTTTCAGAGCTGCGG 477
 OY 618 AGCACTAGTGGGCGCGCGCGCGCATGTTGGGCGCGCGCTGCGCGCAGCGCGCGCTGCG 677
 DB 478 AGCACTAGTGGGCGCGCGCGCGCATGTTGGGCGCGCGCTGCGCGCAGCGCGCGCTGCG 537
 OY 678 GCGGCTGAGAGAGTGTGTGCCAGCGCATGTCGCGCGCTGGGTGGCGAGAACTGCG 737
 DB 538 GCGGCTGAGAGAGTGTGTGCCAGCGCATGTCGCGCGCTGGGTGGCGAGAACTGCG 597

OY	738	CGCGATACGCTTTTAAACCGGATACCGGATACCTGATGCTTCCTCCCTCCAGACT	797
Db	598	CTCGATATCCCTTCAACCCGCTCTCCGGAGACTACTGATGCTTCCTCCCTCCAGATT	657
OY	798	GACCGGCTGCGCTGTGCGCGACATTAAGTGGGGGCCCTTATTTATTTATTTAA	857
Db	658	GAACCGGACGCGCCCGCGACGAGCATTAAGTGGGATGCGCTGTTAT	709
OY	858	TTATATATATTTTGTGAACACGCTGGGAGGCCCTCCCC-GCCTGGGTCGAGGAGTGG	916
Db	709	TTGTTATTAATCTGCTGGAGACCATGAGGATACCTGCCGCTGGGTTGGAGGAGCGG	768
OY	917	TTGTG--GAGGGTGAATGCTCCACACTTCGCTGGAGAGA-----CCTCATCCACCTC	968
Db	769	ATGGGTGATGAGGGCGAGGGGCTCCCGGCTCGGCTGGAGAGAGAGCCGACAGCCCTTC	828
OY	969	TCAGGGGATGGGGGTCT----CCCTCTCGGTGCTCCCTCCGGGGTCCCC--CTGGTGT	1022
Db	829	TCACCTCTGAGAGGGGCTCTCCCTCTCGGTGCTCCCTCGGGTCCCTGGTGGT	888
OY	1023	AGCAGCT---TGTTCTGGGGCGACGACCTGAAT--CCACTCCTACCTCTCATGTT	1076
Db	889	AGCAGCTTAACCTGATCTGAGACCGAGACCTGAATCGACCTCTACTCTTATGTT	948
OY	1077	ACATATTCACGATATCTTGGACAAACAGAGGG-TCGGGAGGGTCTGCTCATTTT	1135
Db	949	ACATATACCCATATCTTTGACAAACAGGGGTTGGGGAGGGTCTGCTTATTTT	1008
OY	1136	TCGTGTGACGAATATCCTATTTATATTTTATACAGCAGTTTGAATATACTTAT	1195
Db	1009	TCGTGTGACGAATCCTATTTTATAT-TTTTAAAGTCAGTTTGAATATACTTAT	1067
OY	1196	TATGAAGTTTTTTTTTAAAGAAAA	1222
Db	1068	TATGAAGTTTTTTTTTAAAAAAA	1094
RESULT	13		
LOCUS	AB005043		
DEFINITION	Homo sapiens mRNA for STAT induced STAT inhibitor-1, complete cds.		
ACCESSION	AB005043		
VERSION	AB005043.1	GI:2443364	
KEYWORDS	STAT induced STAT inhibitor-1.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1082)		
AUTHORS	Minamoto, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-JUN-1997) to the DDBJ/EMBL/GenBank databases. Seq. Info		
REFERENCE	1 (bases 1 to 1082)		
AUTHORS	Minamoto, S., Ikegami, K., Ieno, K., Narazaki, M., Naka, T., Yamamoto, H., Matsumoto, T., Saito, H., Hosoe, S. and Kishimoto, T.		
TITLE	Cloning and functional analysis of new members of STAT induced STAT		
JOURNAL	Inhibitor (SSI) family: SSI-2 and SSI-3		
FEATURES	Biochem. Biophys. Res. Comm. 237, 79-83 (1997)		
source	Location/Qualifiers		
	1..1082		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	54..689		
	/note="SSI-1"		
	/codon_start=1		
	/evidence="experimental		
	/product="STAT induced STAT inhibitor-1"		
	/protein_id="BA22431.1"		
	/db_xref="GI:2443365"		
	/translation="MAAHNOVAADNAVSTAAPRRRPPSSSSSSPAAPARPPCPA		

BASE COUNT	154	a	396	c	316	g	216	t
ORIGIN								
Query Match	55.3%	Score	682.4	DB	9	Length	1082	
Best Local Similarity	83.4%	Pred.	No. 8,2e-114					
Matches	904	Conservative	0	Mismatches	146	Indels	34	Gaps 10:
OY	108	CAGCGACGCCCCGGACGCCTATAGGCCACCCTCCAGCTGGCCCCCTCGAGTAGATGTAG	167					
Db	1	CAGCGACGCCCCGGACGCCTATAGGCCACCCTCCGGCTGGCCCCCTTCGTGTAGATGTAG	60					
OY	168	CACGCAACCAAGTGGACGACGACAATGGATCTCCCGGGCAGACAGAGCCCGACGGCGGT	227					
Db	61	CACACAAACCAAGTGGACGACGACCAATGAAGTCTCCACAGCACAGAGCCCGACGGCGGC	120					
OY	228	CAGAGCCCTCCTGTCTGTCTTTCTGTCCTGACAGCGGGCCCCCGTGTCGCCGCCCT	287					
Db	121	CAGAACCTTCC---TCCCTTCTCTCTCTGCGCCGCGCGCCCCCGCGCGCCGCGCGGT	177					
OY	288	GCCCGGCGGTCCCAAGCCCACCCCTGGCGACATCATATTCCGACACTTCCGCTCCCACT	347					
Db	178	GCCCCGCGGTCCCGGCCCCCGCCCCCGGACAGCACTTCCGACATTCGCTTCCGACG	237					
OY	348	CCGATTACCGCGCGCATACGCGGACACAGCGCGCTCTTGAGACGCTGCGGCTTCTATTGGG	407					
Db	238	CGGATTACCGCGCGCATACGCGGCGACGCGCGCTCTTGAGAGCGCGGATTCTAAGTGGG	297					
OY	408	GACCCCTAAGGTGTGACAGGGGGCGCACAGCGGGTGTGTGCGAGGCCCTGGGCACTTCT	467					
Db	298	GGCCCTTAAGGTGTGACAGGGGGCGCACAGCGGGTGTGTGCGAGGCCCTGGGCACTTCC	357					
OY	468	TGTTGCGGAGACGTGTGTAACGAACTCTTTCGCGCCTCAGCGTGAAGATGGCTTGGG	527					
Db	358	TGTGTGCGGAGACGCGCGACGAGGAACTCTTTCGCGCCTTACGCTGAAGATGGCTTGGG	417					
OY	528	GCCCCACAGAGCATCGCGTGCATTCCAGSGCGGCGCGCTTCCACTTTGAGACGGACGCGG	587					
Db	418	GACCCACAGAGCATCGCGTGCATTCCAGSGCGGCGCGCTTCCACTTGAATGGACGCCG	477					
OY	588	AGACCTTGACATGCTTTTTCAGCTGTGAGAGCACTAGTGGGGGGCGCGGCGCGCATGT	647					
Db	478	AGAGCTTGACATGCTTTTTCAGAGCTGTGAGAGCACTAGTGGGGGGCGCGGCGCGCATGC	537					
OY	648	TGGGGGCCCCCTGCGCGACGCGCGGTGCGAGCGCGCTGTCAGAGACTGTGTGCCAGAGCA	707					
Db	538	TGGGGGCCCCCTGCGCGACGCGCGGTGCGAGCGCGCTGTCAGAGACTGTGTGCCAGAGCA	597					
OY	708	TGCTGTGCGCGCGGTGTGCGAGAACGTGGGCGCGCATTCCTTTAACCCGGTACTCGTG	767					
Db	598	TGCTGTGCGCGCGGTGTGCGAGAACGTGGGCGCGCATTCCTTTAACCCGGTACTCGTG	657					
OY	768	ACTACTAGTGTCTCTCCCTCCAGATCTACCGGGTCCGCTGTGCGCGAGAGATTAAAG	827					
Db	658	ACTACTAGTGTCTCTCTCCCTCCAGATTTACCGGGACGCCCGCGGTGACAGAGCAT	717					
OY	828	TGGGGGCGCTTATTATTCTTTATTATTATTATTATTATTATTATTATTATTATTATTATT	887					
Db	718	TAACTGGGATCCCGTGTATT-----TTGTTATTACTTGCCTGGAACATGTGTGGT	768					
OY	888	GCCCTCCCC--GCTGGGGTGGAGGAGGTGTGG---GAGGGAGAAATGCTCCCACTT	943					
Db	769	AACCTCCCCCGGCTGTGGTGGAGGAGGTGTGGTGTAGGGGGAGAGCGCTCCCGCC	828					
OY	944	CTGGCTGGAGA-----CCTCATCCCACTCTCAGAGGGTGGGGGTGTCT---CCCTCTGTG	994					
Db	829	TGGGCTGGAGACAGGGCGGACAGCCCTTCTCACACTGTGTGAGGGGGTCTCCCTCTGTG	888					
OY	995	GTCGCTCCCTCGGGTCCCCC--CTGGTTTGAAGACT---TGTGTCTGGGGCCAAGACC	1048					

